



CDS: SPAC4F10.02



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General Information

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Systematic Name SPAC4F10.02

Status role inferred from homology

Product aminopeptidase (predicted)

Type CDS

Sequence DNA and Protein

Location

Chromosome 1

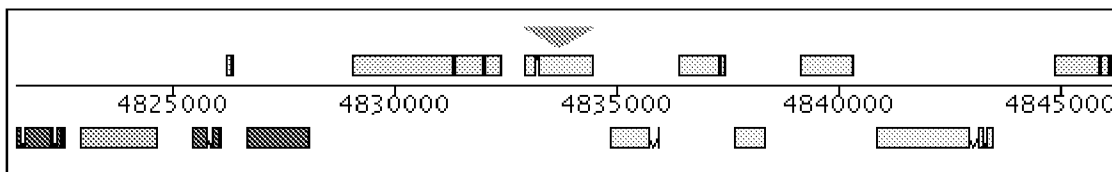
Contig Location 4832929..4834428 (Unspliced length: 1500 bp)

Exons join(4832929..4833160 , 4833257..4834428) (Spliced length: 1404 bp)

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Context Map:



[hus1](#) [SPAC20G4.05c](#) [adfl](#) [SPAC20G4.09](#) [sts1](#) [SPAC20G4.08](#) >SPAC4F10.02< [SPAC4F10.03c](#) [SPAC4F10.04](#)
[SPAC4F10.05c](#) [SPAC4F10.06](#) [atg13](#) [mug126](#)

Curation

Term

conserved eukaryotic family

metallopeptidase

peptidase family M18

similar to *S. cerevisiae* [YHR113W](#)

Other genes annotated to this term

(866 Others)

(7 Others)

(0 Others)

(0 Others)

Predicted Peptide Properties

Mass	51.7 kDa	Amino acids	467
Isoelectric point	pH 5.7	Charge	-6.0
Signal Peptide	Not found		
Transmembrane Domains	0 found		
GPI Anchor	Not found		

Gene Ontology Annotation

Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term
Biological Process		
proteolysis	ISS (PMID:17072883) with Pfam:PF02127	228 others
Cellular Component		
cytoplasm	ISS (PMID:17072883) with SGD:S0000001155	4204 others
cytosol	IDA (PMID:16823372)	2322 others
fungal-type vacuole	ISS (PMID:17072883) with Pfam:PF02127	30 others
Molecular Function		
aspartyl aminopeptidase activity	ISS (PMID:17072883) with SGD:S0000001155	none
metallopeptidase activity	IEA (GOA:spkw GO_REF:0000004) with SP_KW:KW-0482	39 others
zinc ion binding	IEA (GOA:interpro GO_REF:0000002) with InterPro:IPR001948	353 others

Catalytic Activity

EC 3.4.11.- : IUBMB

Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)
 TranscriptomeViewer [SPAC4F10.02 High-resolution view of transcripts in neighbourhood](#)

Literature

Search for in [PubMed](#)

Domain Information

[View Pfam domain structure for this gene product](#)[View SCOP superfamily](#)

DB	Accs	Description
Pfam	PF02127	Aminopeptidase I zinc metalloprotease (M18)
MEROPS	M18.002	MEROPS
InterPro	IPR001948	Peptidase M18, aminopeptidase I
PRINTS	PR00932	Aminopeptidase I zinc metalloprotease (M18) signature

Database Cross-References

DB	Accs	Description
UniProtKB	O36014	Putative aspartyl aminopeptidase (EC 3.4.11.21).
EMBL	CU329670	Schizosaccharomyces pombe chromosome I
EMBL	D89276	Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1794.
Biotwiki	SPAC4F10.02	Biotwiki
NCBI Entrez Gene	SPAC4F10.02	NCBI Entrez Gene
FYSSION	SPAC4F10.02	FYSSION
GermOnline	SPAC4F10.02	GermOnline
NBRP	SPAC4F10.02	Fission yeast strain database, National BioResource Project (Japan)
PIR	T38806	PIR

PIR [T43206](#) PIR
YOGY [SPAC4F10.02](#) Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

Catalytic Activity Release of an N-terminal aspartate or glutamate from a peptide, with a preference for aspartate.
Cofactor Binds 1 zinc ion per subunit (By similarity).
Similarity Belongs to the peptidase M18 family.
Subcellular Location Cytoplasm (By similarity).
Keywords [Aminopeptidase \(10 others\)](#) , [Complete proteome \(4982 others\)](#) , [Cytoplasm \(861 others\)](#) , [Hydrolase \(451 others\)](#) , [Metal-binding \(451 others\)](#) , [Metalloprotease \(21 others\)](#) , [Protease \(90 others\)](#) , [Zinc \(302 others\)](#)

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